

Fig.1.

M V N R S V A F S A F V L I L F V L A I
 1 ATGGTGAATCGGTCGGTTGCGTTCTCCGCGTTCTGTTCTGATCCTTTTCGTGCTCGCCATC

S
 61 TCAGGTTATCAAAATCTTTAGTTCATTTATTGAATATGATAGTATTTATATTCITTTATGG

intron
 D I A S V S G E
 121 TTTTATGTGTTCTGACAAAGTTGCAAAATATTGAGTAGATATCGCATCCGTTAGTGGAGAAC

L C E K A S K T W S G N C G N T G H C D
 181 TATCGGAGAAAGCTAGCAAGACATGGTTCGGGAAACTGTGGCAATACGGGACATTGTGACA

N Q C K S W E G A A H G A C H V R N G K
 241 ACCAATGTAAATCATGGAGGGTGGCGCCCATGGAGCGTGTCTCATGTGCGTAAACGGGAAAC

HindIII
 Q M C F C Y F N C K K A E K L A Q D K L
 301 AGATGTGTTTCTGTACTTCAATTGTAAAAAGCCGAAAGCTTGTCTCAAGACAAACTTA

HindIII
 K A E Q L A Q D K L N A Q K L D R D A K
 361 AAGCCGAACAACCTCGCTCAAGACAAACTTAATGCCCCAAAGCTTGACCGTGTATGCCAAGA

K V V P N V E H P
 421 AAGTGGTTCCAAACGTTGAACATCCG SEQ ID NO 2
 SEQ ID NO 1

Fig.2.

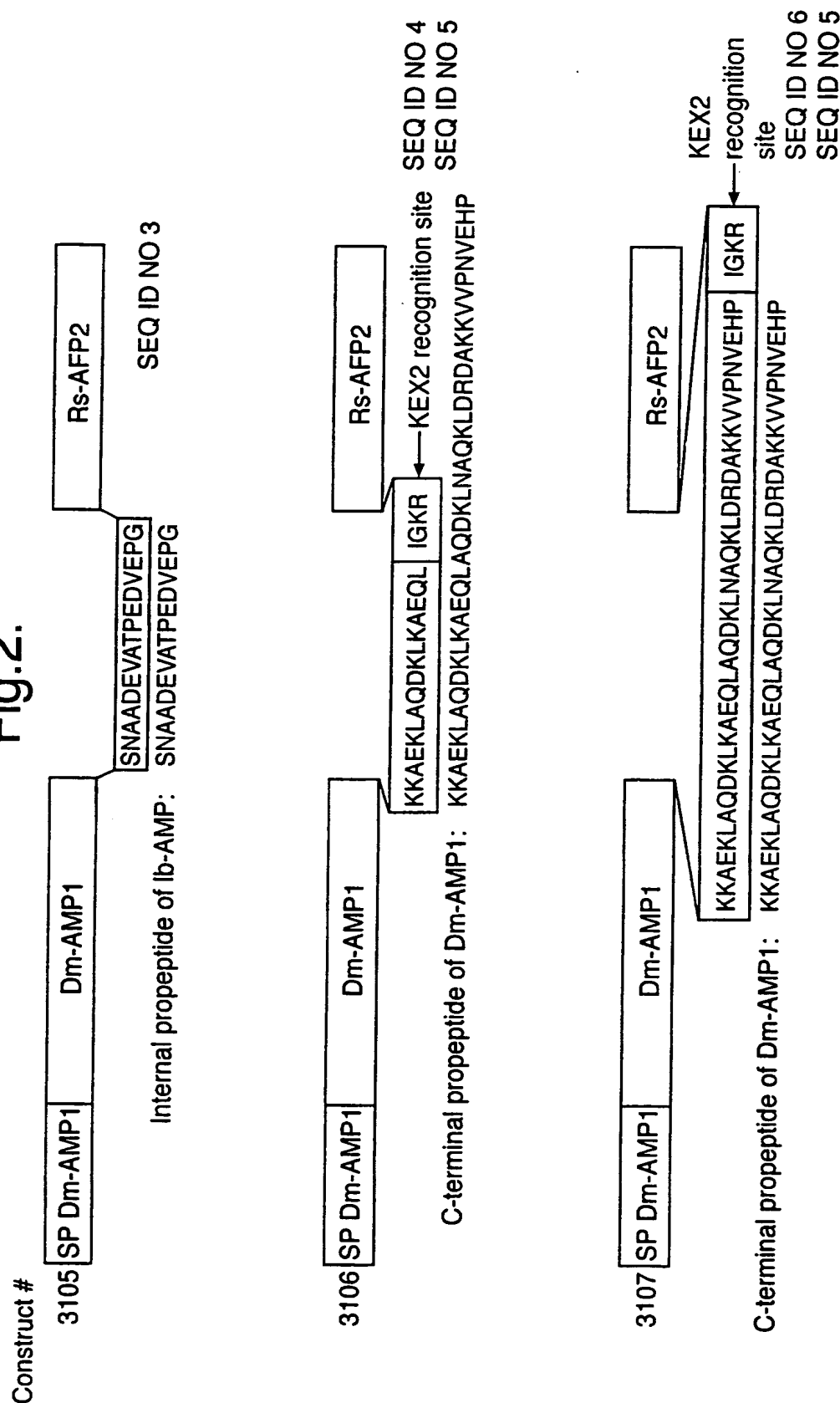
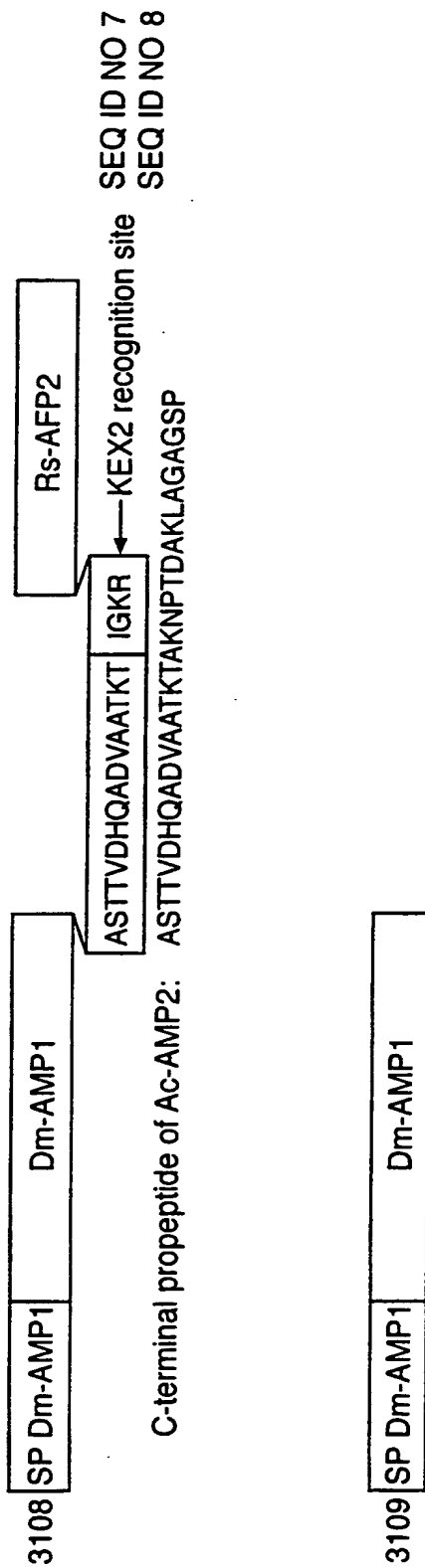
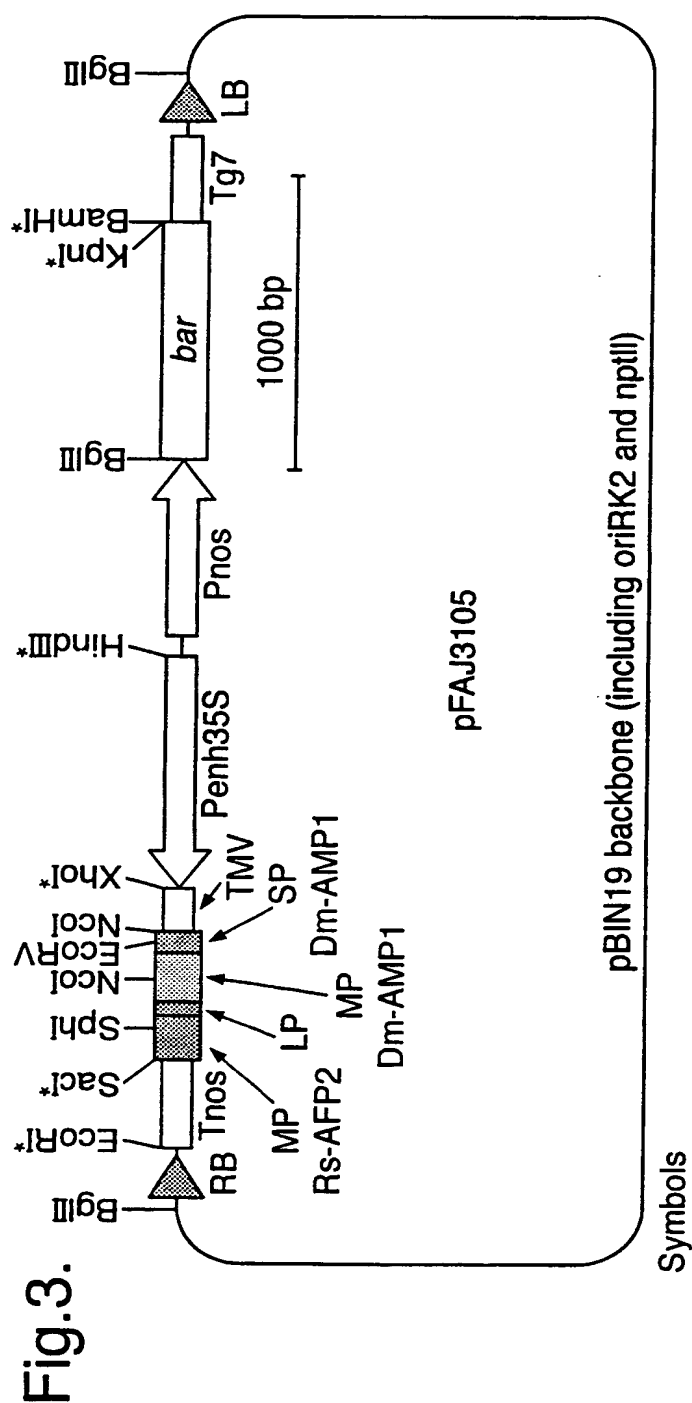
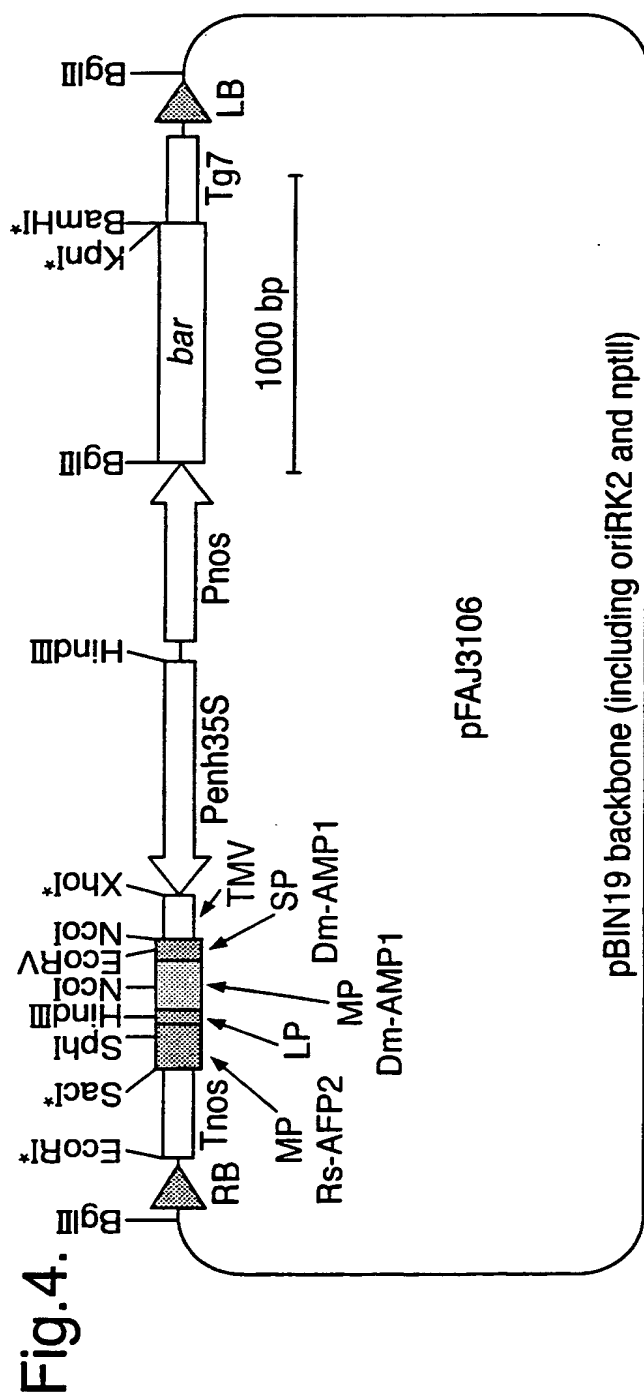


Fig.2 (Cont).





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Symbols

RB: right border of T-DNA

Tnos: terminator of T-DNA nopaline synthase gene

MP Rs-AFP2: mature protein domain of Rs-AFP2

LP: first 16 AA of Dm-AMP1 C-terminal propeptide and subtilisin-like protease recognition site IGKR

MP Dm-AMP1: mature protein domain of Dm-AMP1 cDNA

SP Dm-AMP1: signal peptide domain of Dm-AMP1 cDNA

TMV: tobacco mosaic virus 5' leader sequence

Penh35S: promotor of 35S RNA of cauliflower mosaic virus with duplicated enhancer region

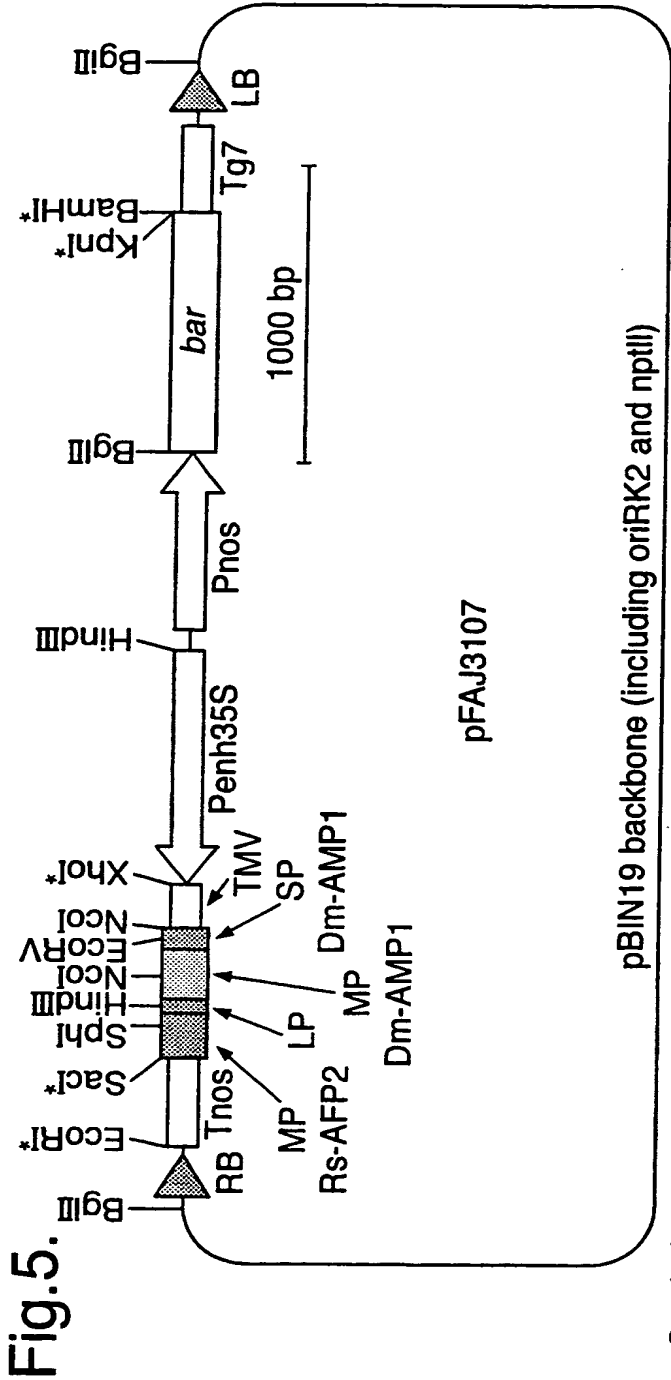
Phos: promotor of T-DNA nopaline synthase gene

bar: basta resistance encoding gene

Tg7: terminator of T-DNA gene 7

LB: left border of T-DNA

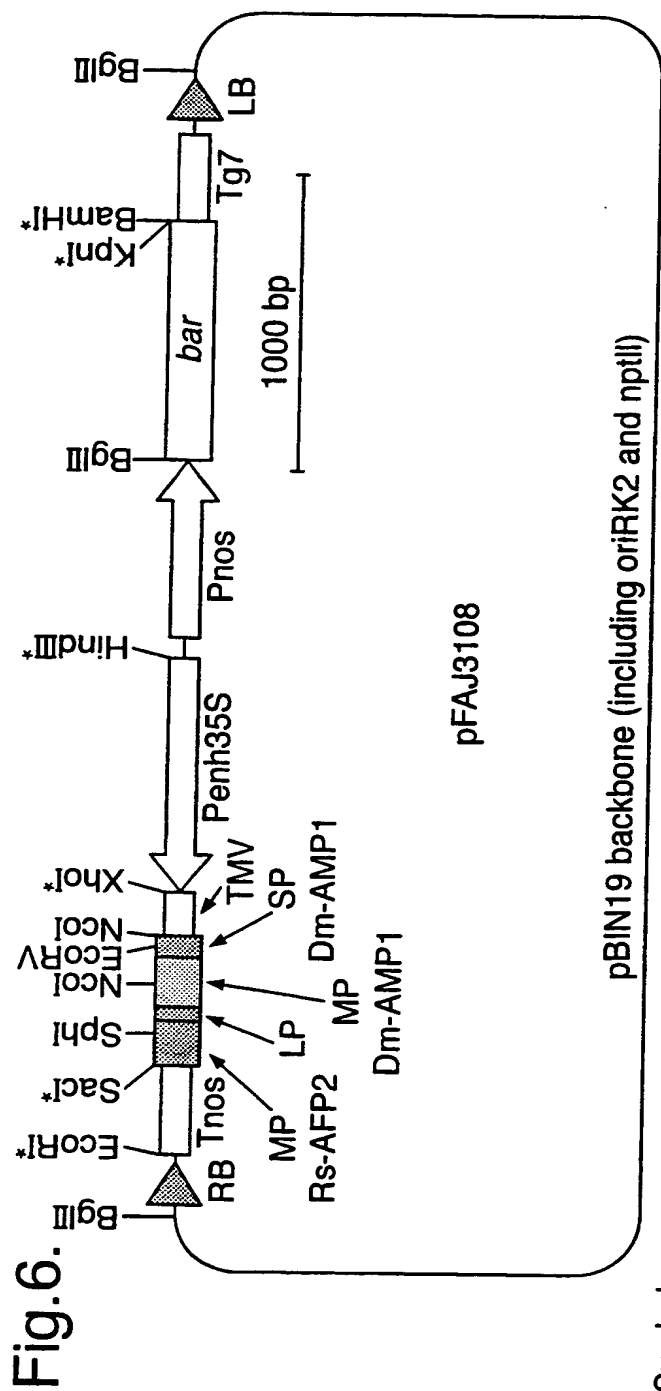
*: unique restriction site



Symbols

- RB: right border of T-DNA
- Tnos: terminator of T-DNA nopaline synthase gene
- MP Rs-AFP2: mature protein domain of Rs-AFP2
- LP: Dm-AMP1 C-terminal propeptide domain and subtilisin-like protease recognition site IGKR
- MP Dm-AMP1: mature protein domain of Dm-AMP1 cDNA
- SP Dm-AMP1: signal peptide domain of Dm-AMP1 cDNA
- TMV: tobacco mosaic virus 5' leader sequence
- Penh35S: promoter of 35S RNA of cauliflower mosaic virus with duplicated enhancer region
- Pnos: promoter of T-DNA nopaline synthase gene
- bar: basta resistance encoding gene
- Tg7: terminator of T-DNA gene 7
- LB: left border of T-DNA
- *: unique restriction site

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Symbols

RB: right border of T-DNA

Tnos: terminator of T-DNA nopaline synthase gene

MP Rs-AFP2: mature protein domain of Rs-AFP2

LP: first 16 AA of Ac-AMP2 C-terminal propeptide domain and subtilisin-like protease recognition site IGKR

MP Dm-AMP1: mature protein domain of Dm-AMP1 cDNA

SP Dm-AMP1: signal peptide domain of Dm-AMP1 cDNA

TMV: tobacco mosaic virus 5' leader sequence

Penh35S: promotor of 35S RNA of cauliflower mosaic virus with duplicated enhancer region

Pnos: promotor of T-DNA nopaline synthase gene

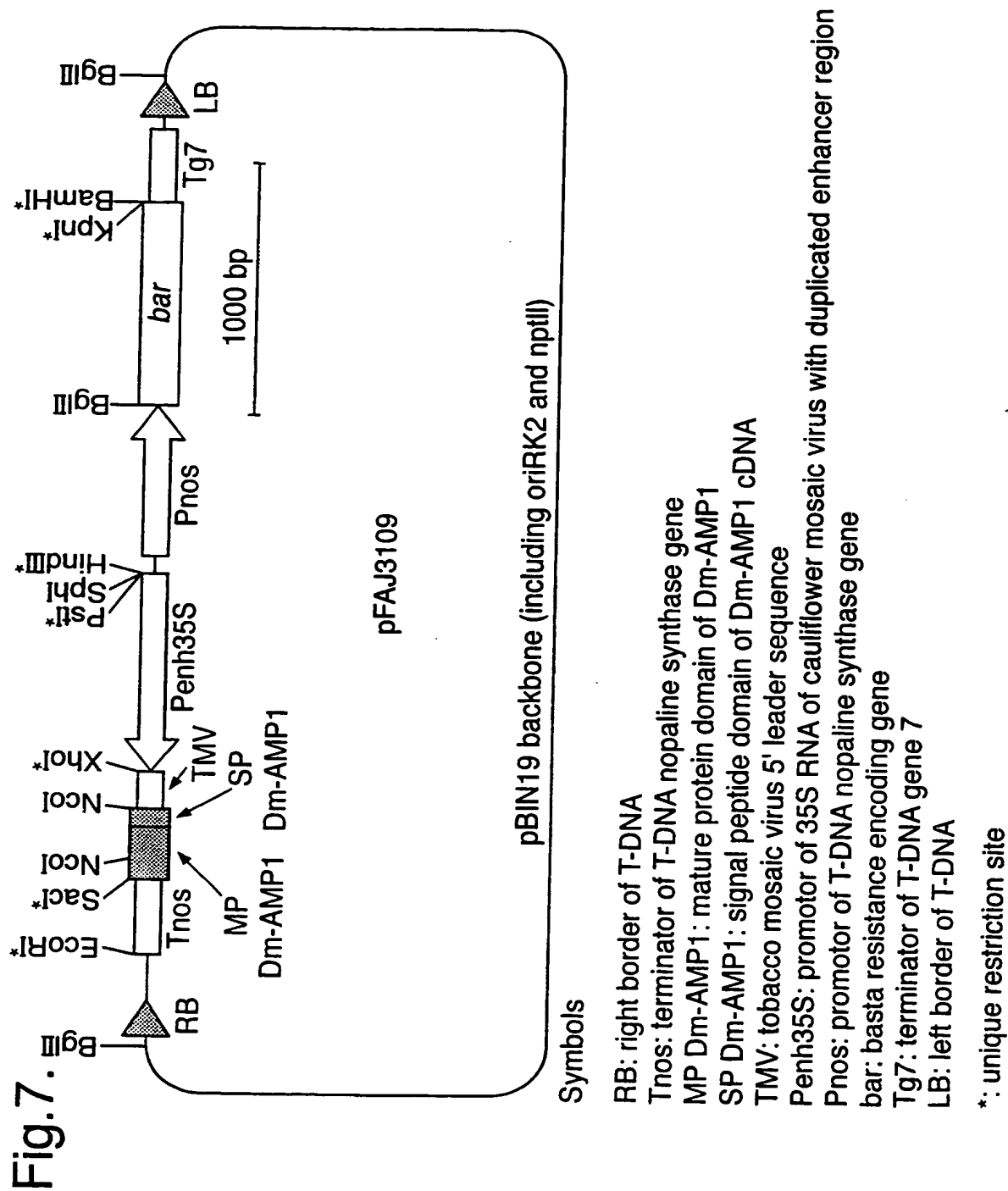
bar: basta resistance encoding gene

Tg7: terminator of T-DNA gene 7

LB: left border of T-DNA

*: unique restriction site

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Fig.8.

pFAJ3105

XhoI
CTCGAGTATTTTACACAATTACCAACAACAACAACAACAACAATTAATTAAT

NcoI
ATTTACAATTACACCATGGTGAATCGGTCGGTTGCGTTCTCCGCGTTCTGATCCTT
M V N R S V A F S A F V L I L

TTCGTGCTCGCCATCTCAGATATCGCATCCGTTAGTGGAGAACTATCGGAGAAAGCTAGC
F V L A I S D I A S V S G E L C E K A S

AAGACGTGGTCGGCAACTGTGGCAACACGGGACATTTGTGACAACCAATGTAAATCATGG
K T W S G N C G N T G H C D N Q C K S W

GAGGTGCGGCCCATGGAGCGTGTCTATGTCGTAACGGAAACACATGTGTTTCTGTTAC
E G A A H G A C H V R N G K H M C F C Y

TTCAATTGTTCCAACGCTGCTGACGAGGTGGCTACCCAGAGGACGTGGAGCCAGGACAG
F N C S N A A D E V A T P E D V E P G Q

AAGTTGTGCCAAAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGC
K L C Q R P S G T W S G V C G N N A C

AAGAATCAGTGCATTTAGACTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCCA
K N Q C I R L E K A R H G S C N Y V F P

SacI
GCTCACAAGTGTATCTGCTACTTTTCCCTTGTTAATAGGAGCTC
A H K C I C Y F P C - -

SEQ ID NO 9
SEQ ID NO 10

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Fig.9.

pFAJ3106XhoI

CTCGAGTATTTTACAAACAATTACCAACAACAACAACAACAACAATTACAATTACT

NcoI

ATTTACAATTACACCATGGTGAATCGGTCGGTTCTCCGGTTCTCGTTCTGATCCTT

M V N R S V A F S A F V L I L

TTCGTGCTCGCCATCTCAGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGC

F V L A I S D I A S V S G E L C E K A S

AAGACGTGTCGGGCAACTGTGGCAACACGGGACATGTGACAACCAATGTAAATCATGG

K T W S G N C G N T G H C D N Q C K S W

GAGGTGCGGCCCATGGAGCGTGTCAATGTCGTAACGGGAAACACATGTGTTTCTGTAC

E G A A H G A C H V R N G K H M C F C Y

TTCAATTGTAAAAAGCCGAAAGCTTGCTCAAGACAAACTTAAAGCCGAACAACATCATC

F N C K K A E K L A Q D K L K A E Q L I

GGAAAGAGGCAGAAAGTTGTGCCAAAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAC

G K R Q K L C Q R P S G T W S G V C G N

AATAACGCATGCAAGAATCAGTGCATTAGACTTGAGAAAGCACGACATGGATCTTGCAAC

N N A C K N Q C I R L E K A R H G S C N

SacI

TATGTCTTCCCAGCTCACAAAGTGTATCTGTACTTTCCCTTGTTAATAGGAGCTC

Y V F P A H K C I C Y F P C - -

SEQ ID NO 11

SEQ ID NO 12

Fig.10.
pFAJ3107

XhoI
CTCGAGTATTTTACAAACAATTACCAACAACAACAACAACAACAACAATTACAATTACT

NcoI
ATTTTACAATTACACCATGGTGAATCGGTGCGTTGCGTTCTCCGCGTTCTGTTCTGATCCCTT
M V N R S V A F S A F V L I L

TTTCGTGCTCGCCATCTCAGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGC
F V L A I S D I A S V S G E L C E K A S

AAGACGTGGTCGGGCAACTGTGGCAACACGGGACATTTGTGACAACCAATGTAAATCATGG
K T W S G N C G N T G H C D N Q C K S W

GAGGTGCGGCCCATGGAGCGTGTCTATGTGCGTAAACGGGAAACACATGTGTTCTGTGTAC
E G A A H G A C H V R N G K H M C F C Y

TTCAATTGTAAAAAGCCGAAAGCTTGCTCAAGACAAACTTAAAGCCGAAACAACCTCGCT
F N C K K A E K L A Q D K L K A E Q L A

CAAGACAAACTTAATGCCCAAAAGCTTGACCGTGTATGCCAAGAAAGTGGTTCCAAACGTT
Q D K L N A Q K L D R D A K K V V P N V

GAACATCCGATCGGAAAGAGGCAGAAAGTTGTGCCAAAGGCCAAGTGGACATGGTCAGGA
E H P I G K R Q K L C Q R P S G T W S G

GTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATTAGACTTGAGAAAGCACGACAT
V C G N N A C K N Q C I R L E K A R H

GGATCTTGCAACTATGTCTTCCAGCTCACAAGTGTATCTGCTACTTTCTCTTGTAAATAG
G S C N Y V F P A H K C I C Y F P C - -

SacI
GAGCTC

SEQ ID NO 15
SEQ ID NO 16

Fig.11. pFAJ3108

XhoI

CTCGAGTATTTTACACAATACCAACAACAACAACAACAACAATACAAATTACT

NcoI

ATTTACAATTACACCATGGTGAATCGGTGGTTGCGTTCTCCGCGTTCGTTCTGATCCTT

M V N R S V A F S A F V L I L

TTCGTGCTCGCCATCTCAGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGC

F V L A I S D I A S V S G E L C E K A S

AAGACGTGGTGGGCAACTGTGGCAACACGGGACATTTGTGACAACCAATGTAAATCATGG

K T W S G N C G N T G H C D N Q C K S W

GAGGGTGGGCCCATGGAGCGTGTATGTGCGTAACGGGAAACACATGTGTTTCTGTAC

E G A A H G A C H V R N G K H M C F C Y

TTCAATTGTGCCAGTACTACTGTGGATCACCAAGCTGATGTTGCTGCCACCAAACTATC

F N C A S T T V D H Q A D V A A T K T I

GGAAAGAGGCAGAAGTTGTGCCAAGGCCAAGTGGGACATGTCAGGAGTCTGTGGAAAC

G K R Q K L C Q R P S G T W S G V C G N

AATAACGCATGCAAGAATCAGTGCATTAGACTTGAGAAAGCACGACATGGATCTTGCAAC

N N A C K N Q C I R L E K A R H G S C N

SacI

TATGTCTTCCAGCTCACAAGTGTATCTGCTACTTTTCCTTGTAAATAGGAGCTC

Y V F P A H K C I C Y F P C - -

SEQ ID NO 17

SEQ ID NO 18

Fig.12.

pFAJ3109

XhoI

CTCGAGTATTTTACAAACAATTACCAACAACAACAACAACAACAATTACAATACT

NcoI

ATTTACAATTACACCATGGTGAATCGGTCGGTTGCGTTCTCCGCGTTCTGATCCTT
M V N R S V A F S A F V L I L

TTCGTGCTCGCCATCTCAGATATCGCATCCGTTAGTGGAGAACTATCGGAGAAAGCTAGC
F V L A I S D I A S V S G E L C E K A S

AAGACGTGTCGGGCAACTGTGGCAACACGGGACATTGTGACAACCAATGTAATCATGG
K T W S G N C G N T G H C D N Q C K S W

GAGGTGCGGCCCATGGAGCGTGTCAATGCGTAATGGGAACACATGTCTCTGTAC
E G A A H G A C H V R N G K H M C F C Y

SacI

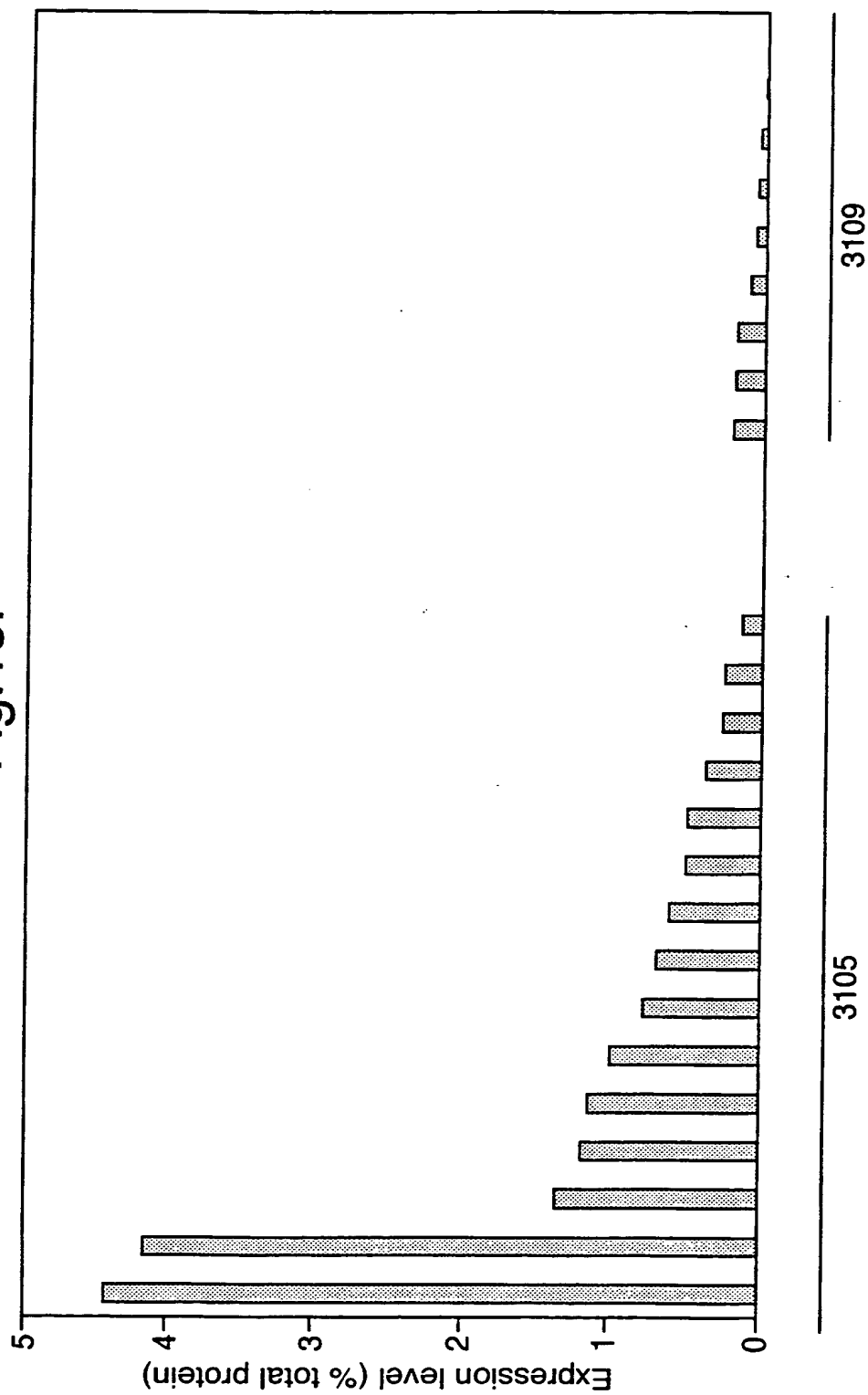
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SEQ ID NO 19

SEQ ID NO 20

F N C

Fig. 13.



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Fig.14A.

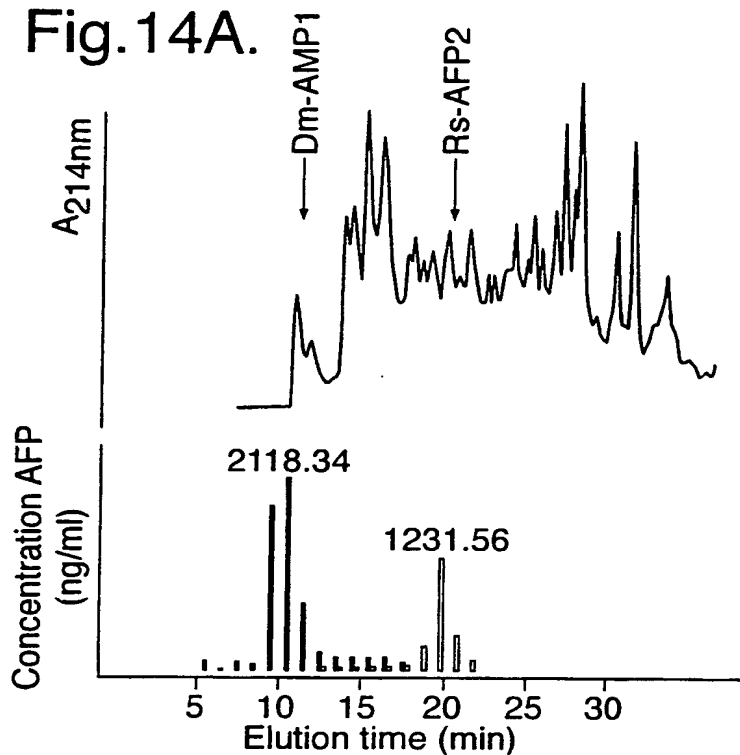
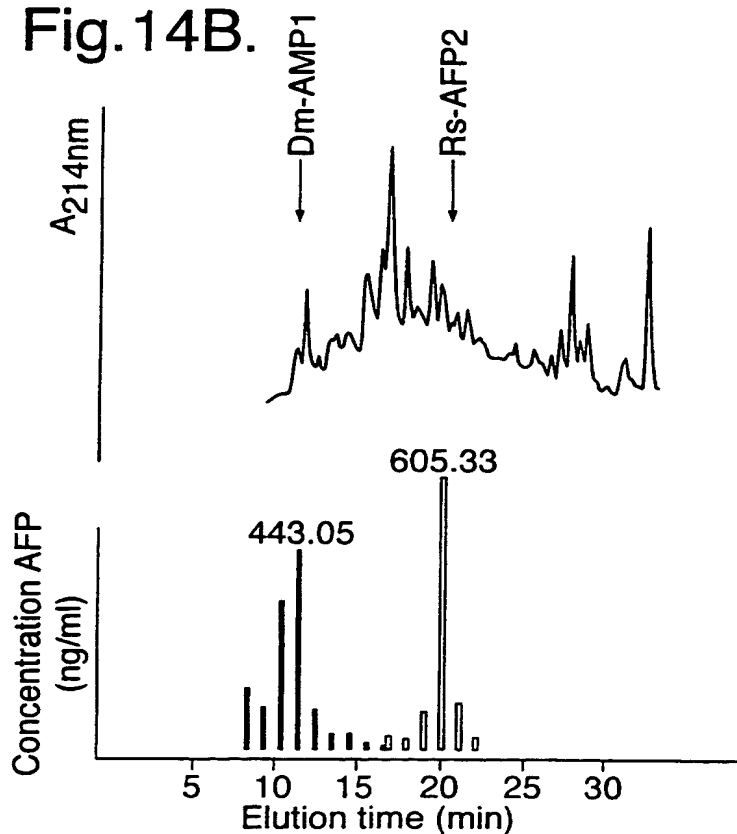


Fig.14B.



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Fig.15.

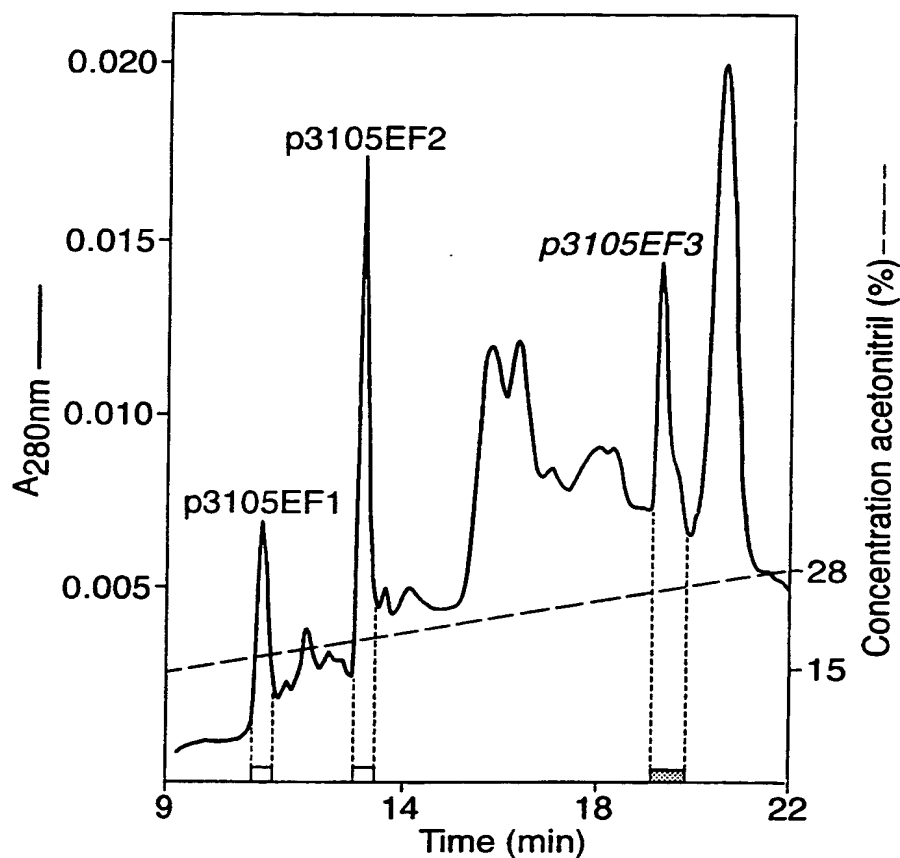


Fig.17.

Construct

Sequence

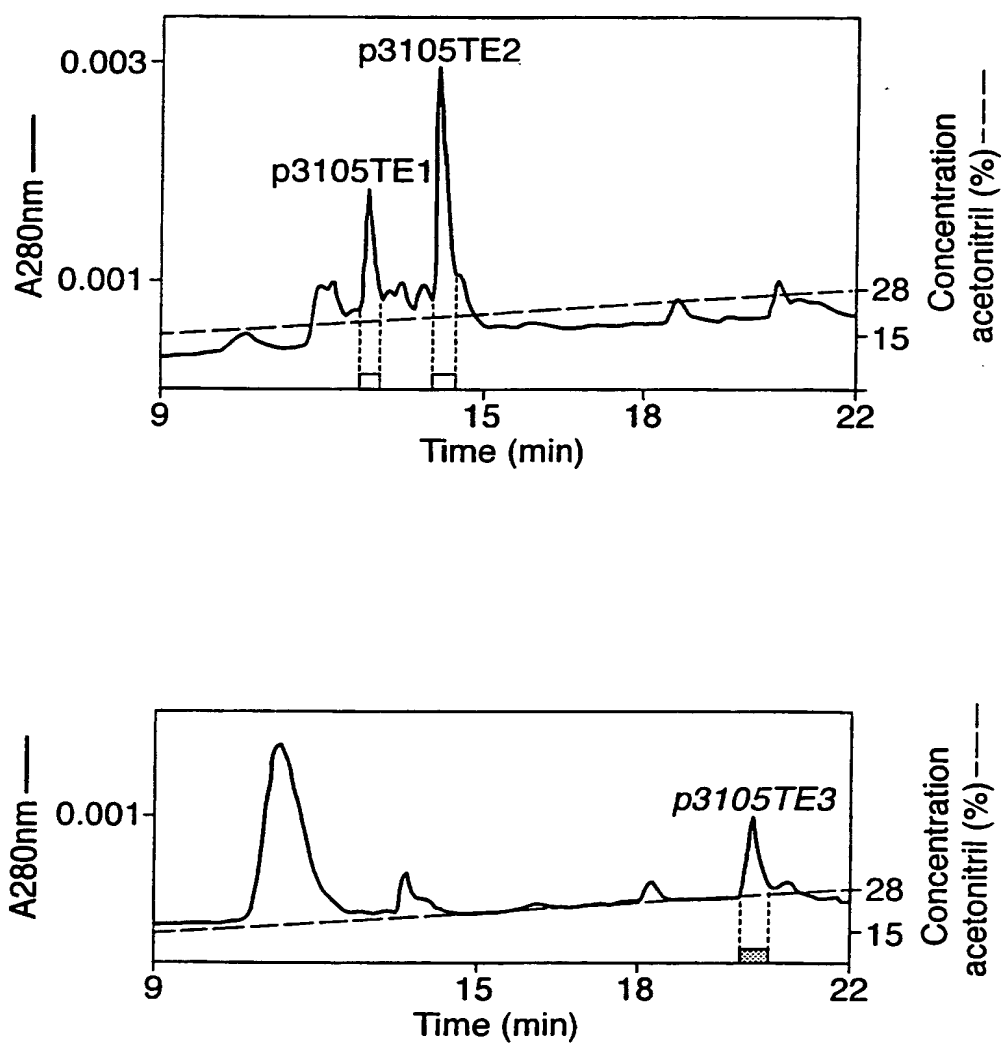
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pFAJ3106 MVN VSGELC FNCKKAEKLAQDKLKAEQLIGKROKL...FPC

pFAJ3108 MVN VSGELC FNCASTTVDHQADVAATKTIGKROKL...FPC

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Fig.16.



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Fig.18.

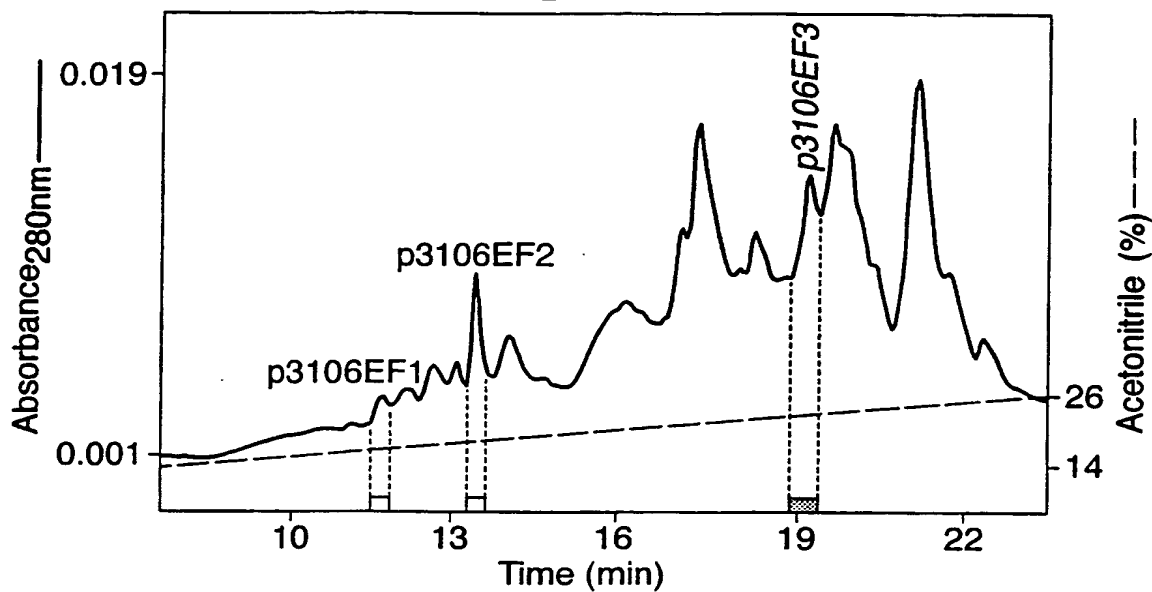


Fig.19.

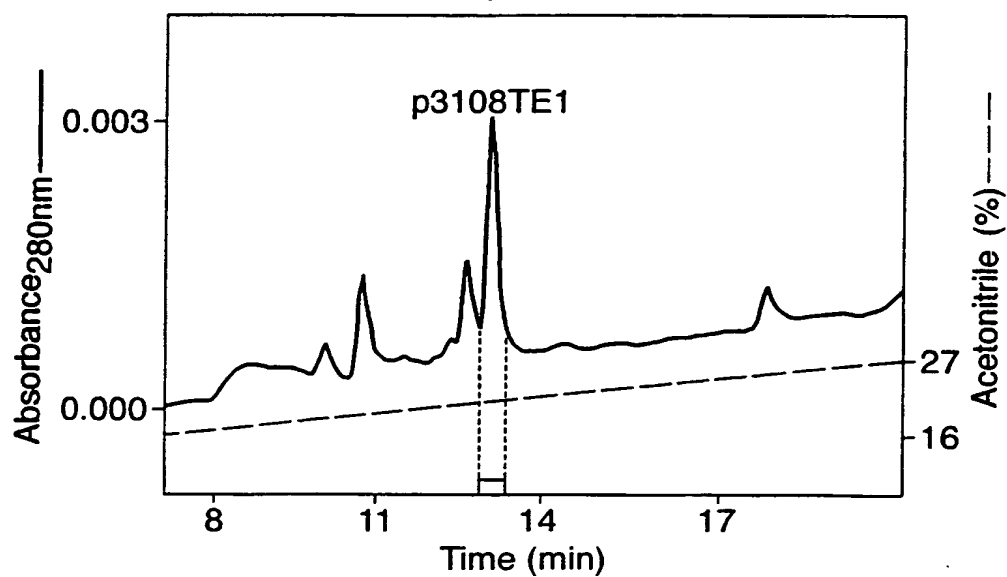
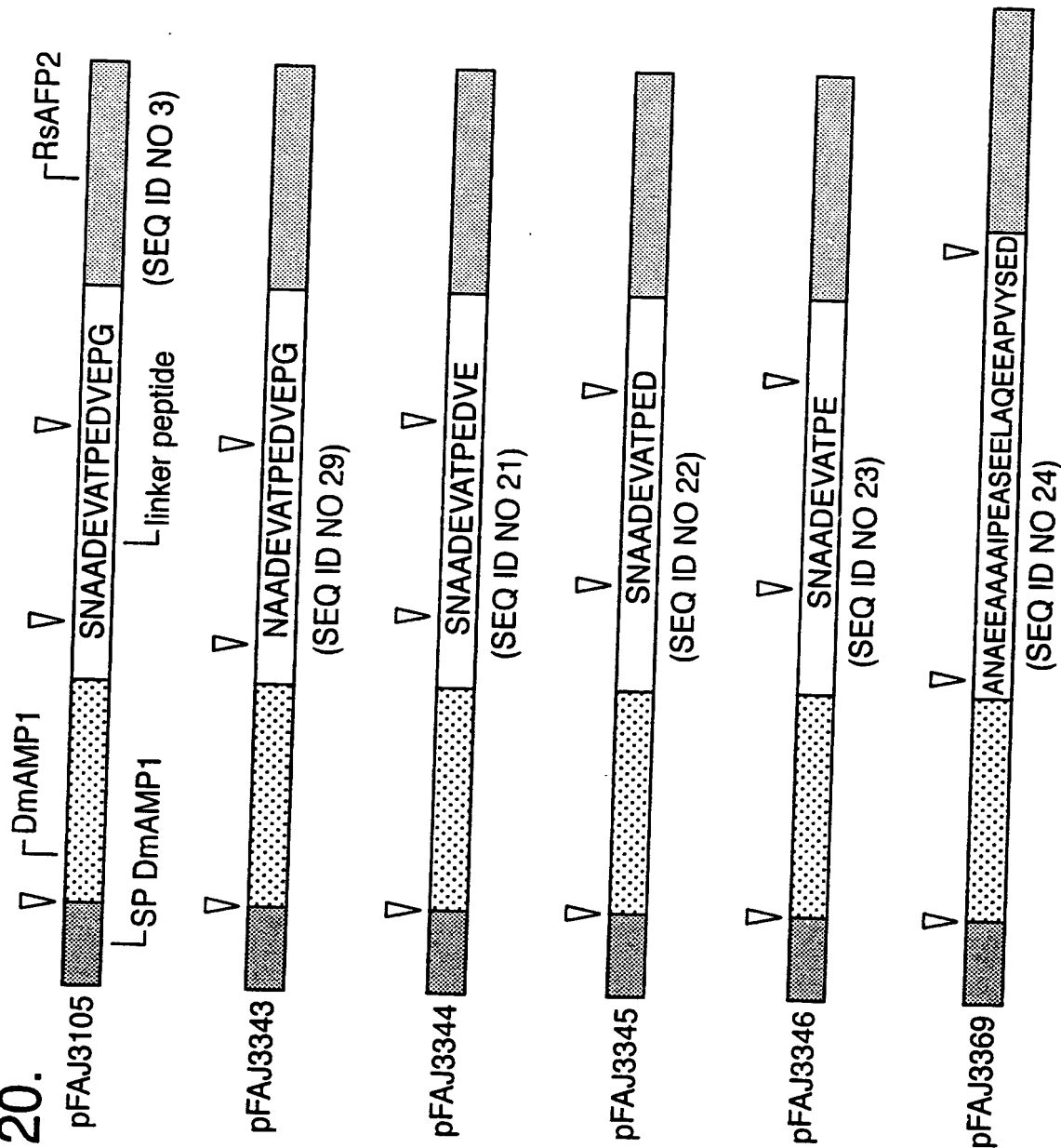


Fig.20.



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Fig.21.

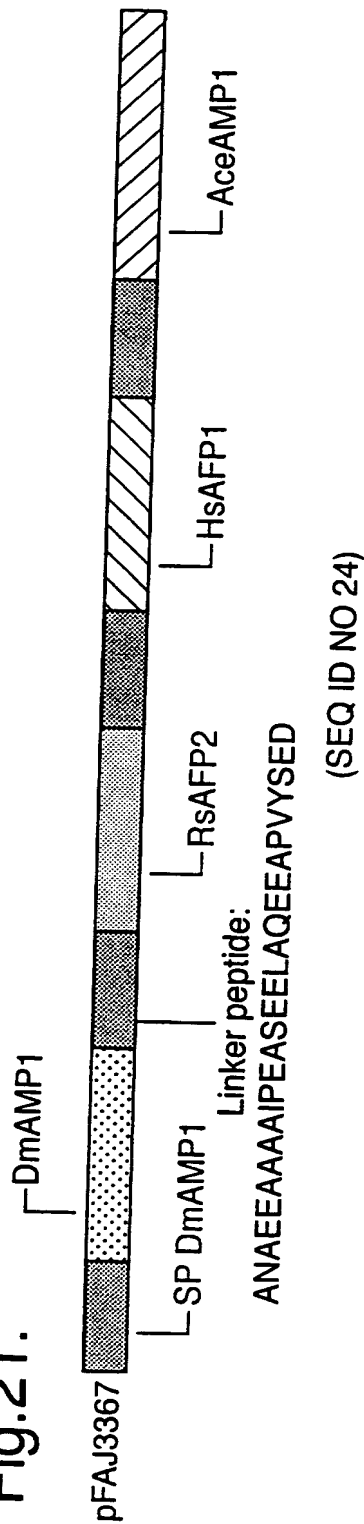


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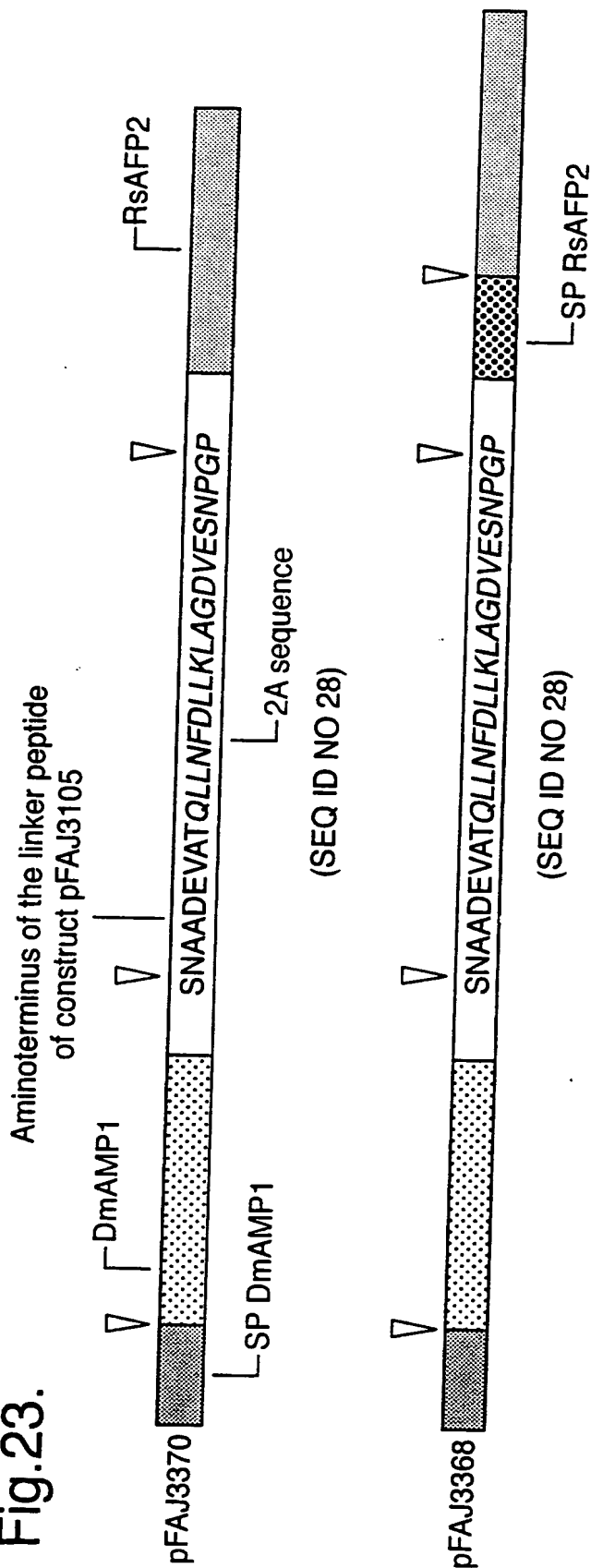
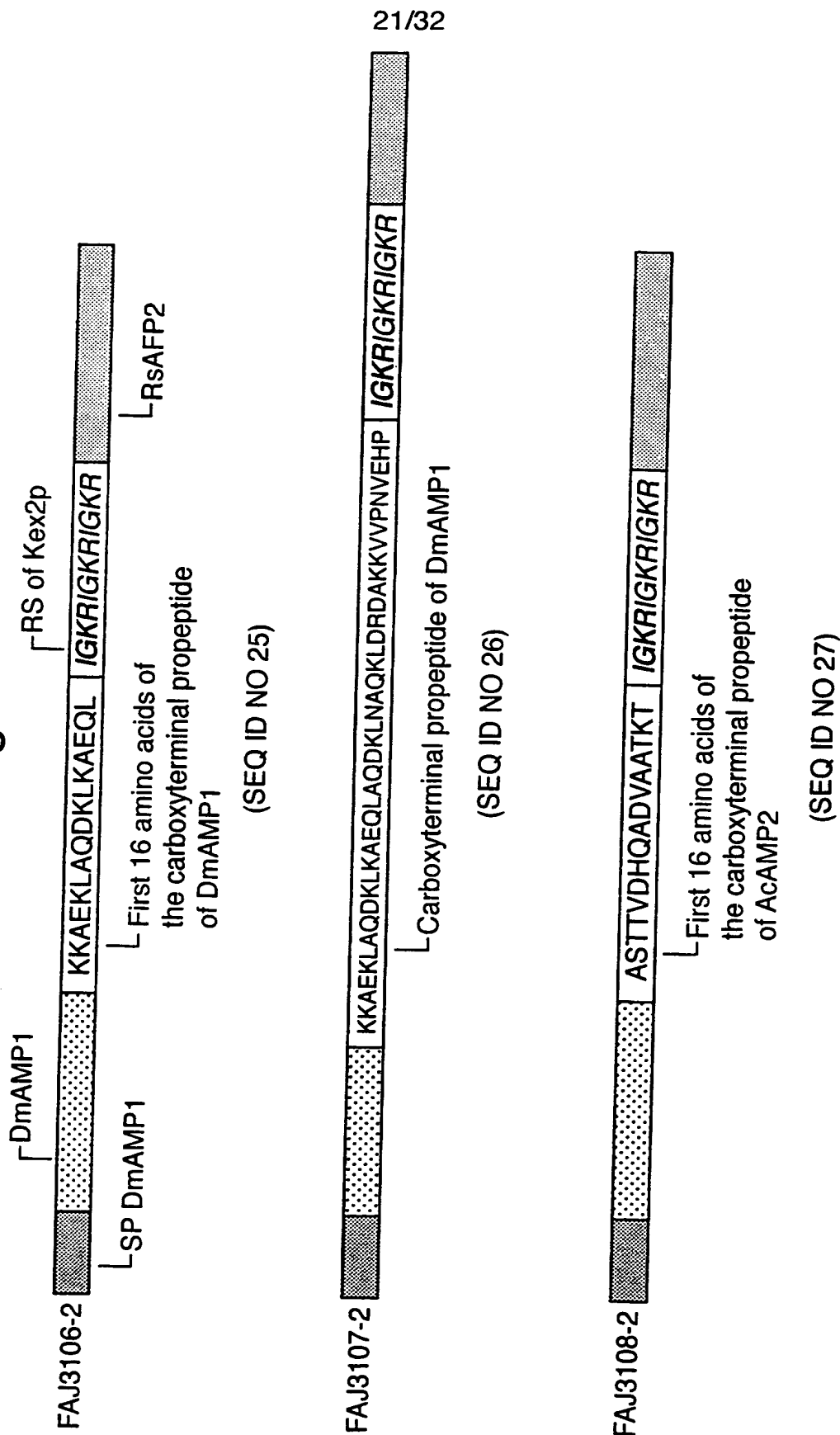


Fig.22.



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Fig.24.

pFAJ3343

NcoI

CCATGGTGAATCGGTCGGTTGCGTTCTCCGCGTTTCGTTCTGATCCTTTTCGTGCTCGCC
M V N R S V A F S A F V L I L F V L A

ATCTCAGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACGTGGTTCG
I S D I A S V S G E L C E K A S K T W S

GGCAACTGTGGCAACACGGGACATTGTGACAACCAATGTAAATCATGGGAGGGGTGCGGCT
G N C G N T G H C D N O C K S W E G A A

CACGGAGCGTGTTCATGTGCGTAACGGGAAACACATGTGTTTCTGTTACTTCAATTGTAAC
H G A C H V R N G K H M C F C Y F N C N

GCGGCCGACGAGGTGGCTACCCCAGAGGACGTGGAACCTGGTCAGAAGTTGTGCCAAAGG
A A D E V A T P E D V E P G O K L C O R

CCAAGTCGTACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT
P S R T W S G V C G N N N A C K N O C I

AGACTTGAGAAAGCACGACATGGATCTTGCAACTATCGTTTCCCAGCTCACAAGTGTATC
R L E K A R H G S C N Y R F P A H K C I

SacI

TGCTACTTTCCTTGTTAATAGGAGCTC
C Y F P C - -

(SEQ ID NO 30)

(SEQ ID NO 31)

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pFAJ3344

Fig.25.

NcoI

CCATGGTGAATCGGTTCGGTTGCGTTCTCCGCGTTCGTTCTGATCCTTTTCGTGCTCGCC
M V N R S V A F S A F V L I L F V L A

ATCTCAGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACGTGGTTCG
I S D I A S V S G E L C E K A S K T W S

GGCAACTGTGGCAACACGGGACATTGTGACAACCAATGTAAATCATGGGAGGGTGCGGCT
G N C G N T G H C D N O C K S W E G A A

CACGGAGCGTGTTCATGTGCGTAACGGGAAACACATGTGTTTCTGTTACTTCAATTGTTC
H G A C H V R N G K H M C F C Y F N C S

AACGCGGCCGACGAGGTGGCTACCCCAGAGGACGTGGAACAGAAGTTGTGCCAAAGGCCA
N A A D E V A T P E D V E Q K L C O R P

AGTCGTACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAGA
S R T W S G V C G N N N A C K N O C I R

CTTGAGAAAGCACGACATGGATCTTGCAACTATCGTTTCCCAGCTCACAAGTGTATCTGC
L E K A R H G S C N Y R F P A H K C I C

TACTTTCCTTGTTAATAGGAGCTC (SEQ ID NO 32)
Y F P C - - (SEQ ID NO 33)

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pFAJ3345

Fig.26.

NcoI

CCATGGTGAATCGGTCGGTTGCGTTCTCCGCGTTCTGATCCTTTTCGTGCTCGCC
M V N R S V A F S A F V L I L F V L A

ATCTCAGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACGTGGTCC
I S D I A S V S G E L C E K A S K T W S

GGCAACTGTGGCAACACGGGACATTGTGACAACCAATGTAAATCATGGGAGGGTGCGGCT
G N C G N T G H C D N O C K S W E G A A

CACGGAGCGTGTTCATGTGCGTAACGGGAAACACATGTGTTTCTGTTACTTCAATTGTTCC
H G A C H V R N G K H M C F C Y F N C S

AACGCGGCCGACGAGGTGGCTACCCCAGAGGACCAGAAGTTGTGCCAAAGGCCAAGTCGT
N A A D E V A T P E D O K L C O R P S R

ACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAGACTTGAG
T W S G V C G N N N A C K N O C I R L E

AAAGCACGACATGGATCTTGCAACTATCGTTTCCCAGCTCACAAGTGTATCTGCTACTTT
K A R H G S C N Y R F P A H K C I C Y F

SacI

CCTTGTTAATAGGAGCTC

P C - -

(SEQ ID NO 34)

(SEQ ID NO 35)

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pFAJ3346

Fig.27.

NcoI

CCATGGTGAATCGGTCGGTTGCGTTCTCCGCGTTCTGATCCTTTTCGTGCTCGCC
M V N R S V A F S A F V L I L F V L A

ATCTCAGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACGTGGTCG
I S D I A S V S G E L C E K A S K T W S

GGCAACTGTGGCAACACGGGACATTGTGACAACCAATGTAAATCATGGGAGGGTGCGGCT
G N C G N T G H C D N O C K S W E G A A

CACGGAGCGTGTTCATGTGCGTAACGGGAAACACATGTGTTTCTGTTACTTCAATTGTTCC
H G A C H V R N G K H M C F C Y F N C S

AACGCGGCCGACGAGGTGGCTACCCCAGAGCAGAAGTTGTGCCAAAGGCCAAGTCGTACA
N A A D E V A T P E O K L C O R P S R T

TGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAGACTTGAGAAA
W S G V C G N N N A C K N O C I R L E K

GCACGACATGGATCTTGCAACTATCGTTTCCAGCTCACAAGTGTATCTGCTACTTTTCCT
A R H G S C N Y R F P A H K C I C Y F P

SacI

TGTTAATAGGAGCTC

(SEQ ID NO 36)

C - -

(SEQ ID NO 37)

F014F50-920E9260

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pFAJ3369

Fig.28.

NcoI

CCATGGTGAATCGGTCGGTTGCGTTCTCCGCGTTCTGATCCTTTTCGTGCTCGCC

M V N R S V A F S A F V L I L F V L A

ATCTCAGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACGTGGTTCG

I S D I A S V S G E L C E K A S K T W S

GGCAACTGTGGCAACACGGGACATTGTGACAACCAATGTAAATCATGGGAGGGTGCGGCT

G N C G N T G H C D N O C K S W E G A A

CACGGAGCGTGTTCATGTGCGTAACGGGAAACACATGTGTTTCTGTTACTTCAATTGTGCT

H G A C H V R N G K H M C F C Y F N C A

AACGCTGAGGAAGCTGCTGCTGCTATTCTGAAGCTTCTGAAGAACTTGCTCAAGAAGAA

N A E E A A A A I P E A S E E L A Q E E

GCTCCTGTGTACAGTGAAGATCAGAAGTTGTGCCAAAGGCCAAGTCGTACATGGTCAGGA

A P V Y S E D O K L C O R P S R T W S G

GTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAGACTTGAGAAAGCACGACAT

V C G N N N A C K N O C I R L E K A R H

GGATCTTGCAACTATCGTTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGTTAATAG

G S C N Y R F P A H K C I C Y F P C - -SacI

GAGCTC

(SEQ ID NO 38)

(SEQ ID NO 39)

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Fig.29.

pFAJ3367NcoI

CCATGGTGAATCGGTCGGTTGCGTTCTCCGCGTTCGTTCTGATCCTTTTCGTGCTCGCC
 M V N R S V A F S A F V L I L F V L A

ATCTCAGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACGTGGTTCG
 I S D I A S V S G E L C E K A S K T W S

GGCAACTGTGGCAACACGGGACATTGTGACAACCAATGTAAATCATGGGAGGGTGC GGCT
G N C G N T G H C D N O C K S W E G A A

CACGGAGCGTGT CATGTGCGTAACGGGAAACACATGTGTTTCTGTTACTTCAACTGCGCT
H G A C H V R N G K H M C F C Y F N C A

AACGCTGAGGAAGCTGCTGCTGCTATTCTGAAGCTTCTGAAGAACTTGCTCAAGAAGAA
 N A E E A A A A I P E A S E E L A Q E E

GCTCCTGTGTACAGTGAAGATCAGAAGTTGTGCCAAAGGCCAAGTCGTACATGGTCAGGA
 A P V Y S E D O K L C O R P S R T W S G

GTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAGACTTGAGAAAGCACGACAT
V C G N N N A C K N O C I R L E K A R H

GGATCTTGCAACTATCGTTTCCCAGCTCACAAGTGTATCTGCTACTTCCCTTGTGCGAAT
G S C N Y R F P A H K C I C Y F P C A N

GCTGAAGAAGCTGCTGCTGCTATTCTGAAGCTTCTGAAGAACTTGCTCAAGAAGAAGCA
 A E E A A A A I P E A S E E L A Q E E A

CCGGTTTACTCTGAAGATGACGGAGTGAAGCTCTGCGACGTGCCATCCGGAACCTGGTCC
 P V Y S E D D G V K L C D V P S G T W S

GGAACTGCGGTTCTCCAGCAAGTGCAGCCAACAATGCAAGGACAGGGAGCACTTCGCT
G H C G S S S K C S Q Q C K D R E H F A

TACGGAGGAGCTTGCCACTACCAATTC CATCCGTTGAAGTGCTTCTGCAAGAGGCAATGC
Y G G A C H Y Q F P S V K C F C K R Q C

GCTAACGCTGAGGAAGCTGCTGCTGCTATTCTGAAGCTTCTGAAGAACTTGCTCAAGAA
 A N A E E A A A A I P E A S E E L A Q E

GAAGCTCCTGTGTACAGTGAAGATCAGAACATATGCCCAAGGGTTAATCGAATTGTGACA
 E A P V Y S E D O N I C P R V N R I V T

CCCTGTGTGGCCTACGGAAGGGCACCAATCGCCCCATGCTGCAGAGCCCTGAAC
P C V A Y G L G R A P I A P C C R A L N

GATCTACGGTTTGTGAATACTAGAAACCTACGACGTGCTGCATGCCGCTGCCTCGTAGGG
D L R F V N T R N L R R A A C R C L V G

GTAGTGAACCGGAACCCCGGTCTGAGACGAAACCCTAGATTT CAGAACATTCTCGTGAT
V V N R N P G L R R N P R F Q N I P R D

TGTCGCAACACCTTTGTTCGTCCCTTCTGGTGGCGTCCAAGAATTCAATGCGGCAGGATT
C R N T F V R P F W W R P R I Q C G R I

SacI

AACTAATAGAGCTC

N - -

(SEQ ID NO 40)

(SEQ ID NO 41)

SUBSTITUTE SHEET (RULE 26)

T04T50-920E9260

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Fig.30.

pFAJ3106-2NcoI

CCATGGTGAATCGGTCGGTTGCGTTCTCCGCGTTTCGTTCTGATCCTTTTCGTGCTCGCC
M V N R S V A F S A F V L I L F V L A

ATCTCAGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACGTGGTTCG
I S D I A S V S G E L C E K A S K T W S

GGCAACTGTGGCAACACGGGACATTGTGACAACCAATGTAAATCATGGGAGGGTGCGGCT
G N C G N T G H C D N O C K S W E G A A

CACGGAGCGTGTTCATGTGCGTAACGGGAAACACATGTGTTTCTGTTACTTCAATTGTAAA
H G A C H V R N G K H M C F C Y F N C K

AAAGCCGAAAAGCTTGCTCAAGACAACTTAAAGCCGAACAACTCATCGGAAAGAGGATC
K A E K L A Q D K L K A E Q L I G K R I

GGAAAGAGGATCGGAAAGAGGCAGAAAGTTGTGCCAAAGGCCAAGTCGTACATGGTCAGGA
G K R I G K R O K L C O R P S R T W S G

GTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAGACTTGAGAAAGCACGACAT
V C G N N N A C K N O C I R L E K A R H

GGATCTTGCAACTATCGTTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGTTAATAG
G S C N Y R F P A H K C I C Y F P C - -

SacI

GAGCTC

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(SEQ ID NO 43)

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Fig.31.

pFAJ3107-2NcoI

CCATGGTGAATCGGTCGGTTGCGTTCTCCGCGTTCGTTCTGATCCTTTTCGTGCTCGCC
M V N R S V A F S A F V L I L F V L A

ATCTCAGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACGTGGTTCG
I S D I A S V S G E L C E K A S K T W S

GGCAACTGTGGCAACACGGGACATTGTGACAACCAATGTAAATCATGGGAGGGTGCGGCT
G N C G N T G H C D N O C K S W E G A A

CACGGAGCGTGTTCATGTGCGTAACGGGAAACACATGTGTTTCTGTTACTTCAATTGTAAA
H G A C H V R N G K H M C F C Y F N C K

AAAGCCGAAAAGCTTGCTCAAGACAACTTAAAGCCGAACAACTCGCTCAAGACAACTT
K A E K L A Q D K L K A E Q L A Q D K L

AATGCCCAAAAGCTTGACCGTGATGCCAAGAAAGTGGTTCCAAACGTTGAACATCCGATC
N A Q K L D R D A K K V V P N V E H P I

GGAAAGAGGATCGGAAAGAGGATCGGAAAGAGGCAGAAGTTGTGCCAAAGGCCAAGTCGT
G K R I G K R I G K R O K L C O R P S R

ACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAGACTTGAG
T W S G V C G N N N A C K N O C I R L E

AAAGCACGACATGGATCTTGCAACTATCGTTTCCCAGCTCACAAGTGTATCTGCTACTT
K A R H G S C N Y R F P A H K C I C Y F

SacI

TCCTTGTTAATAGGAGCTC

(SEQ ID NO 44)

P C - -

(SEQ ID NO 45)

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pFAJ3108-2

Fig.32.

NcoI

CCATGGTGAATCGGTCGGTTGCGTTCTCCGCGTTTCGTTCTGATCCTTTTCGTGCTCGCC
M V N R S V A F S A F V L I L F V L A

ATCTCAGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACGTGGTTCG
I S D I A S V S G E L C E K A S K T W S

GGCAACTGTGGCAACACGGGACATTGTGACAACCAATGTAAATCATGGGAGGGTGCGGCT
G N C G N T G H C D N O C K S W E G A A

CACGGAGCGTGTTCATGTGCGTAACGGGAAACACATGTGTTTCTGTTACTTCAATTGTGCC
H G A C H V R N G K H M C F C Y F N C A

AGTACTACTGTGGATCACCAAGCTGATGTTGCTGCCACCAAACTATCGGAAAGAGGATC
S T T V D H Q A D V A A T K T I G K R I

GGAAAGAGGATCGGAAAGAGGCAGAAGTTGTGCCAAAGGCCAAGTCGTACATGGTCAGGA
G K R I G K R O K L C O R P S R T W S G

GTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAGACTTGAGAAAGCACGACAT
V C G N N N A C K N O C I R L E K A R H

GGATCTTGCAACTATCTGTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGTTAATAG
G S C N Y R F P A H K C I C Y F P C - -

SacI

GAGCTC

(SEQ ID NO 46)

(SEQ ID NO 47)

FOI 50-92029260

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pFAJ3370

Fig.33.

NcoI

CCATGGTGAATCGGTCGGTTGCGTTCTCCGCGTTTCGTTCTGATCCTTTTCGTGCTCGCC

M V N R S V A F S A F V L I L F V L A

ATCTCAGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACGTGGTCTG

I S D I A S V S G E L C E K A S K T W S

GGCAACTGTGGCAACACGGGACATTGTGACAACCAATGTAAATCATGGGAGGGTGCGGCT

G N C G N T G H C D N O C K S W E G A A

CACGGAGCGTGTTCATGTGCGTAACGGGAAACACATGTGTTTCTGTTACTTCAATTGTTCC

H G A C H V R N G K H M C F C Y F N C S

AACGCGGCCGACGAGGTGGCTACCCAGCTGTTGAATTTTGACCTTCTTAAGCTTGCGGGA

N A A D E V A T Q L L N F D L L K L A G

GACGTGAGTCCAACCCTGGGCCCCAGAAGTTGTGCCAAAGGCCAAGTCGTACATGGTCA

D V E S N P G P O K L C O R P S R T W S

GGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAGACTTGAGAAAGCACGA

G V C G N N N A C K N O C I R L E K A R

CATGGATCTTGCAACTATCGTTTCCCAGCTCACAAGTGTATCTGCTACTTTTCCTTGTTAA

H G S C N Y R F P A H K C I C Y F P C -

SacI

TAGGAGCTC

(SEQ ID NO 48)

(SEQ ID NO 49)

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pFAJ3368

Fig.34.

NcoI

CCATGGTGAATCGGTCGGTTGCGTTCTCCGCGTTTCGTTCTGATCCTTTTCGTGCTCGCC
M V N R S V A F S A F V L I L F V L A

ATCTCAGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACGTGGTCG
I S D I A S V S G E L C E K A S K T W S

GGCAACTGTGGCAACACGGGACATTGTGACAACCAATGTAAATCATGGGAGGGTGCGGCT
G N C G N T G H C D N O C K S W E G A A

CACGGAGCGTGTTCATGTGCGTAACGGGAAACACATGTGTTTCTGTTACTTCAATTGTTCC
H G A C H V R N G K H M C F C Y F N C S

AACGCGGCCGACGAGGTGGCTACCCAGCTGTTGAATTTTGACCTTCTTAAGCTTGCGGGA
N A A D E V A T Q L L N F D L L K L A G

GACGTGAGTCCAACCCTGGGCCCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTT
D V E S N P G P M A K F A S I I A L L F

GCTGCTCTTGTTCTTTTTTGCTGCTTTTGAAGCACCAACAATGGTGGAAGCACAGAAGTTG
A A L V L F A A F E A E T M V E A O K L

TGCCAAAGGCCAAGTCGTACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAAT
C O R P S R T W S G V C G N N N A C K N

CAGTGCATTAGACTTGAGAAAGCACGACATGGATCTTGCAACTATCGTTTCCCAGCTCAC
O C I R L E K A R H G S C N Y R F P A H

SacI

AAGTGTATCTGCTACTTTCCTTGTTAATAGGAGCTC

(SEQ ID NO 50)

K C I C Y F P C - -

(SEQ ID NO 51)

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